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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/834,998A

DATE: 07/30/2002

TIME: 15:05:20

Input Set : A:\0399.2004-002SEQLIST.TXT
 Output Set: N:\CRF3\07302002\I834998A.raw

4 <110> APPLICANT: Gaxiola, Roberto A.
 5 Fink, Gerald R.
 6 Alper, Seth L.
 8 <120> TITLE OF INVENTION: Proton Transporters And Uses In Plants
 11 <130> FILE REFERENCE: 0399.2004-002
 13 <140> CURRENT APPLICATION NUMBER: US 09/834,998A
 14 <141> CURRENT FILING DATE: 2001-04-13
 16 <150> PRIOR APPLICATION NUMBER: US 09/644,039
 17 <151> PRIOR FILING DATE: 2000-08-22
 19 <150> PRIOR APPLICATION NUMBER: US 60/164,808
 20 <151> PRIOR FILING DATE: 1999-11-10
 22 <160> NUMBER OF SEQ ID NOS: 5
 24 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 538
 28 <212> TYPE: PRT
 29 <213> ORGANISM: Artificial Sequence
 31 <220> FEATURE:
 33 <223> OTHER INFORMATION: Arabidopsis - AtNhxl
 35 <400> SEQUENCE: 1
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 38 His Ala Ser Val Val Ala Leu Asn Leu Phe Val Ala Leu Leu Cys Ala
 39 20 25 30
 40 Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn Arg Trp Met Asn Glu
 41 35 40 45
 42 Ser Ile Thr Ala Leu Leu Ile Gly Leu Gly Thr Gly Val Thr Ile Leu
 43 50 55 60
 44 Leu Ile Ser Lys Gly Lys Ser Ser His Leu Leu Val Phe Ser Glu Asp
 45 65 70 75 80
 46 Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala Gly Phe
 47 85 90 95
 48 Gln Val Lys Lys Gln Phe Phe Arg Asn Phe Val Thr Ile Met Leu
 49 100 105 110
 50 Phe Gly Ala Val Gly Thr Ile Ile Ser Cys Thr Ile Ile Ser Leu Gly
 51 115 120 125
 52 Val Thr Gln Phe Phe Lys Lys Leu Asp Ile Gly Thr Phe Asp Leu Gly
 53 130 135 140
 54 Asp Tyr Leu Ala Ile Gly Ala Ile Phe Ala Ala Thr Asp Ser Val Cys
 55 145 150 155 160
 56 Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Leu Leu Tyr Ser Leu
 57 165 170 175
 58 Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Val Val Val Phe

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59	180	185	190
60	Asn Ala Ile Gln Ser Phe Asp Leu Thr His Leu Asn His Glu Ala Ala		
61	195	200	205
62	Phe His Leu Leu Gly Asn Phe Leu Tyr Leu Phe Leu Leu Ser Thr Leu		
63	210	215	220
64	Leu Gly Ala Ala Thr Gly Leu Ile Ser Ala Tyr Val Ile Lys Lys Leu		
65	225	230	235
66	Tyr Phe Gly Arg His Ser Thr Asp Arg Glu Val Ala Leu Met Met Leu		240
67	245	250	255
68	Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu Phe Asp Leu Ser Gly		
69	260	265	270
70	Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met Ser His Tyr Thr Trp		
71	275	280	285
72	His Asn Val Thr Glu Ser Ser Arg Ile Thr Thr Lys His Thr Phe Ala		
73	290	295	300
74	Thr Leu Ser Phe Leu Ala Glu Thr Phe Ile Phe Leu Tyr Val Gly Met		
75	305	310	315
76	320	325	330
77	Asp Ala Leu Asp Ile Asp Lys Trp Arg Ser Val Ser Asp Thr Pro Gly		335
78	340	345	350
79	Thr Ser Ile Ala Val Ser Ser Ile Leu Met Gly Leu Val Met Val Gly		
80	355	360	365
81	Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu Ala Lys		
82	370	375	380
83	Lys Asn Gln Ser Glu Lys Ile Asn Phe Asn Met Gln Val Val Ile Trp		
84	385	390	395
85	400	405	410
86	Trp Ser Gly Leu Met Arg Gly Ala Val Ser Met Ala Leu Ala Tyr Asn		
87	415	420	425
88	430	435	440
89	445	450	455
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94	520	525	530
95	535		
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97	<211> LENGTH: 669		
98	<212> TYPE: PRT		
99	<213> ORGANISM: Artificial Sequence		

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111 <220> FEATURE:
 112 <223> OTHER INFORMATION: Human - HsNhe-6
 114 <400> SEQUENCE: 2
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 117 Ser Ser Pro Arg Ala Arg Arg Leu Met Arg Pro Leu Trp Leu Leu Leu
 118 20 25 30
 119 Ala Val Gly Val Phe Asp Trp Ala Gly Ala Ser Asp Gly Gly Gly Gly
 120 35 40 45
 121 Glu Ala Arg Ala Met Asp Glu Glu Ile Val Ser Glu Lys Gln Ala Glu
 122 50 55 60
 123 Glu Ser His Arg Gln Asp Ser Ala Asn Leu Leu Ile Phe Ile Leu Leu
 124 65 70 75 80
 125 Leu Thr Leu Thr Ile Leu Thr Ile Trp Leu Phe Lys His Arg Arg Ala
 126 85 90 95
 127 Arg Phe Leu His Glu Thr Gly Leu Ala Met Ile Tyr Gly Leu Leu Val
 128 100 105 110
 129 Gly Leu Val Leu His Tyr Gly Ile His Val Pro Ser Asp Val Asn Asn
 130 115 120 125
 131 Val Thr Leu Ser Cys Glu Val Gln Ser Ser Pro Thr Thr Leu Leu Val
 132 130 135 140
 133 Thr Phe Asp Pro Glu Val Phe Phe Asn Ile Leu Leu Pro Pro Ile Ile
 134 145 150 155 160
 135 Phe Tyr Ala Gly Tyr Ser Leu Lys Arg Arg His Phe Phe Arg Asn Leu
 136 165 170 175
 137 Gly Ser Ile Leu Ala Tyr Ala Phe Leu Gly Thr Ala Ile Ser Cys Phe
 138 180 185 190
 139 Val Ile Gly Ser Ile Met Tyr Gly Gly Val Thr Leu Met Lys Val Thr
 140 195 200 205
 141 Gly Gln Leu Ala Gly Asp Phe Tyr Phe Thr Asp Cys Leu Leu Phe Gly
 142 210 215 220
 143 Ala Ile Val Ser Ala Thr Asp Pro Val Thr Val Leu Ala Ile Phe His
 144 225 230 235 240
 145 Glu Leu Gln Val Asp Val Glu Leu Tyr Ala Leu Leu Phe Gly Glu Ser
 146 245 250 255
 147 Val Leu Asn Asp Ala Val Ala Ile Val Leu Ser Ser Ser Ile Val Ala
 148 260 265 270
 149 Tyr Gln Pro Ala Gly Asp Asn Ser His Thr Phe Asp Val Thr Ala Met
 150 275 280 285
 151 Phe Lys Ser Ile Gly Ile Phe Leu Gly Ile Phe Ser Gly Ser Phe Ala
 152 290 295 300
 153 Met Gly Ala Ala Thr Gly Val Val Thr Ala Leu Val Thr Lys Phe Thr
 154 305 310 315 320
 155 Lys Leu Arg Glu Phe Gln Leu Leu Glu Thr Gly Leu Phe Phe Leu Met
 156 325 330 335
 157 Ser Trp Ser Thr Phe Leu Leu Ala Glu Ala Trp Gly Phe Thr Gly Val
 158 340 345 350
 159 Val Ala Val Leu Phe Cys Gly Ile Thr Gln Ala His Tyr Thr Tyr Asn
 160 355 360 365

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161 Asn Leu Ser Thr Glu Ser Gln His Arg Thr Lys Gln Leu Phe Glu Leu
162      370           375           380
163 Leu Asn Phe Leu Ala Glu Asn Phe Ile Phe Ser Tyr Met Gly Leu Thr
164      385           390           395           400
165 Leu Phe Thr Phe Gln Asn His Val Phe Asn Pro Thr Phe Val Val Gly
166          405           410           415
167 Ala Phe Val Ala Ile Phe Leu Gly Arg Ala Ala Asn Ile Tyr Pro Leu
168          420           425           430
169 Ser Leu Leu Leu Asn Leu Gly Arg Arg Ser Lys Ile Gly Ser Asn Phe
170          435           440           445
171 Gln His Met Met Met Phe Ala Gly Leu Arg Gly Ala Met Ala Phe Ala
172          450           455           460
173 Leu Ala Ile Arg Asp Thr Ala Thr Tyr Ala Arg Gln Met Met Phe Ser
174      465           470           475           480
175 Thr Thr Leu Leu Ile Val Phe Phe Thr Val Trp Val Phe Gly Gly Gly
176          485           490           495
177 Thr Thr Ala Met Leu Ser Cys Leu His Ile Arg Val Gly Val Asp Ser
178          500           505           510
179 Asp Gln Glu His Leu Gly Val Pro Glu Asn Glu Arg Arg Thr Thr Lys
180          515           520           525
181 Ala Glu Ser Ala Trp Leu Phe Arg Met Trp Tyr Asn Phe Asp His Asn
182          530           535           540
183 Tyr Leu Lys Pro Leu Leu Thr His Ser Gly Pro Pro Leu Thr Thr Thr
184      545           550           555           560
185 Leu Pro Ala Cys Cys Gly Pro Ile Ala Arg Cys Leu Thr Ser Pro Gln
186          565           570           575
187 Ala Tyr Glu Asn Gln Glu Leu Lys Asp Asp Asp Ser Asp Leu Ile
188          580           585           590
189 Leu Asn Asp Gly Asp Ile Ser Leu Thr Tyr Gly Asp Ser Thr Val Asn
190          595           600           605
191 Thr Glu Pro Ala Thr Ser Ser Ala Pro Arg Arg Phe Met Gly Asn Ser
192          610           615           620
193 Ser Glu Asp Ala Leu Asp Arg Glu Leu Ala Phe Gly Asp His Glu Leu
194      625           630           635           640
195 Val Ile Arg Gly Thr Arg Leu Val Leu Pro Met Asp Asp Ser Glu Pro
196          645           650           655
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198          660           665
201 <210> SEQ ID NO: 3
202 <211> LENGTH: 633
203 <212> TYPE: PRT
204 <213> ORGANISM: Artificial Sequence
206 <220> FEATURE:
207 <223> OTHER INFORMATION: Yeast - ScNhxl
209 <400> SEQUENCE: 3
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213          20          25           30

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214 Ser Pro Asp Leu Pro Gly Ser Asp Asp Pro Ile Ala Gly Asp Pro Asp
215      35          40          45
216 Val Asp Leu Asn Pro Val Thr Glu Glu Met Phe Ser Ser Trp Ala Leu
217      50          55          60
218 Phe Ile Met Leu Leu Leu Ile Ser Ala Leu Trp Ser Ser Tyr Tyr
219 65          70          75          80
220 Leu Thr Gln Lys Arg Ile Arg Ala Val His Glu Thr Val Leu Ser Ile
221      85          90          95
222 Phe Tyr Gly Met Val Ile Gly Leu Ile Ile Arg Met Ser Pro Gly His
223      100         105         110
224 Tyr Ile Gln Asp Thr Val Thr Phe Asn Ser Ser Tyr Phe Phe Asn Val
225      115         120         125
226 Leu Leu Pro Pro Ile Ile Leu Asn Ser Gly Tyr Glu Leu Asn Gln Val
227      130         135         140
228 Asn Phe Phe Asn Asn Met Leu Ser Ile Leu Ile Phe Ala Ile Pro Gly
229 145         150         155         160
230 Thr Phe Ile Ser Ala Val Val Ile Gly Ile Ile Leu Tyr Ile Trp Thr
231      165         170         175
232 Phe Leu Gly Leu Glu Ser Ile Asp Ile Ser Phe Ala Asp Ala Met Ser
233      180         185         190
234 Val Gly Ala Thr Leu Ser Ala Thr Asp Pro Val Thr Ile Leu Ser Ile
235      195         200         205
236 Phe Asn Ala Tyr Lys Val Asp Pro Lys Leu Tyr Thr Ile Ile Phe Gly
237      210         215         220
238 Glu Ser Leu Leu Asn Asp Ala Ile Ser Ile Val Met Phe Glu Thr Cys
239 225         230         235         240
240 Gln Lys Phe His Gly Gln Pro Ala Thr Phe Ser Ser Val Phe Glu Gly
241      245         250         255
242 Ala Gly Leu Phe Leu Met Thr Phe Ser Val Ser Leu Leu Ile Gly Val
243      260         265         270
244 Leu Ile Gly Ile Leu Val Ala Leu Leu Leu Lys His Thr His Ile Arg
245      275         280         285
246 Arg Tyr Pro Gln Ile Glu Ser Cys Leu Ile Leu Leu Ile Ala Tyr Glu
247      290         295         300
248 Ser Tyr Phe Phe Ser Asn Gly Cys His Met Ser Gly Ile Val Ser Leu
249 305         310         315         320
250 Leu Phe Cys Gly Ile Thr Leu Lys His Tyr Ala Tyr Tyr Asn Met Ser
251      325         330         335
252 Arg Arg Ser Gln Ile Thr Ile Lys Tyr Ile Phe Gln Leu Leu Ala Arg
253      340         345         350
254 Leu Ser Glu Asn Phe Ile Phe Ile Tyr Leu Gly Leu Glu Leu Phe Thr
255      355         360         365
256 Glu Val Glu Leu Val Tyr Lys Pro Leu Leu Ile Ile Val Ala Ala Ile
257      370         375         380
258 Ser Ile Cys Val Ala Arg Trp Cys Ala Val Phe Pro Leu Ser Gln Phe
259 385         390         395         400
260 Val Asn Trp Ile Tyr Arg Val Lys Thr Ile Arg Ser Met Ser Gly Ile
261      405         410         415
262 Thr Gly Glu Asn Ile Ser Val Pro Asp Glu Ile Pro Tyr Asn Tyr Gln

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/834,998A

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TIME: 15:05:21

Input Set : A:\0399.2004-002SEQLIST.TXT

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